#9

SEQUENCE LISTING

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Aizenstein, Brian
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Atiles, Myrta
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de Arruda Indig, Monika
Law, Scott
Mast, Andrea
Marshall, David
Miller, Carolyn
Oldenberg, Mary
Rasmussen, Eric
Schneiders, Jennifer

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Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
        35                  40                  45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
    50                  55                  60

Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
65                  70                  75                  80

Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
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Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
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Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
        115                 120                 125

Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
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Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
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Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
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Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
            180                 185                 190

Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
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Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
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Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
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Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
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Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
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Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
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Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
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Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
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Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
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Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
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Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
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Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
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Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
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Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
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Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu
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His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
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Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
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Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
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Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
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Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
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Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
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Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
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Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
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Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
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Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
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Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
725 730 735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
785 790 795 800

Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
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35 40 45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
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Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu
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Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg
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Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys
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Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu
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Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp
245 250 255

Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu
260 265 270

Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu
275 280 285

Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
290 295 300

Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu
305 310 315 320

Leu Ala Leu Ala Gly Ala Trp Glu Gly Arg Leu His Arg Ala Gln Asp
325 330 335

Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala
340 345 350

Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro
355 360 365

Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
370 375 380

Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
385 390 395 400

Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys
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Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val
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Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val
435 440 445

Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Glu Ala
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Glu Val Arg Gln Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
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485 490 495

Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser
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Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
515 520 525

Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
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Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His
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Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
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Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
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Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Val Leu Val Val Leu
595 600 605

Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
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Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln
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Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met
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Ser Ala His Arg Leu Ser Gly Glu Leu Ser Ile Pro Tyr Glu Glu Ala
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Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala
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Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val
725 730 735

Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
740 745 750

Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Arg Leu Phe
755 760 765

Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp
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Glu Leu Val Leu Glu Ala Pro Lys Asp Arg Ala Glu Arg Val Ala Ala
785 790 795 800

Leu Ala Lys Glu Val Met Glu Gly Val Trp Pro Leu Gln Val Pro Leu
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Glu Val Glu Val Gly Leu Gly Glu Asp Trp Leu Ser Ala Lys Glu
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Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
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Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
130 135 140

Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
145 150 155 160

Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
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Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
195 200 205

Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg
210 215 220

Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp
225 230 235 240

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Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg
260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
275 280 285

Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
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Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
305 310 315 320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg
325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
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Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
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Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
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Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly
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Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
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Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
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Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
675 680 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
690 695 700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
725 730 735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
770 775 780

Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785 790 795 800

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35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val
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Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala
65 70 75 80

Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
85 90 95

Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu
100 105 110

Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys
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Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp
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Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly
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Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
165 170 175

Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn
180 185 190

Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu
195 200 205

Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val
210 215 220

Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa
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Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val
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260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
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Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
290 295 300

Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
305 310 315 320

Leu Leu Ala Leu Ala Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa
325 330 335

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Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa
355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
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Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385 390 395 400

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Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu
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Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
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Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
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Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
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Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu
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580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala
595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
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Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
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Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
675 680 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
690 695 700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
725 730 735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala
785 790 795 800

Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
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gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600

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gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240

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<210> 11

<211> 962

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 11
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ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

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aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420

accgccgaca aagaccttta ccagcttctt tccgaccgca tccacgtcct ccaccccgag 480

gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600

ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660

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ga 962

<210> 12

<211> 1600

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 12

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gccggtgcag gcggtctacg gcttcgccaa gagcctcctc aaggccctca aggaggacgg 180

ggacgcggtg atcgtggtct ttgacgccaa ggccccctcc ttccgccacg aggcctacgg 240

ggggtacaag gcgggccggg cccccacgcc ggaggacttt ccccggcaac tcgccctcat 300

caaggagctg gtggacctcc tggggctggc gcgcctcgag gtcccgggct acgaggcgga 360

cgacgtcctg gccagcctgg ccaagaaggc ggaaaaggag ggctacgagg tccgcatcct 420

caccgccgac aaagaccttt accagctcct ttccgaccgc atccacgtcc tccaccccga 480

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gaacctggac cggctgaagc ccgccatccg ggagaagatc ctggcccaca tggacgatct 720

gaagctctcc tgggacctgg ccaaggtgcg caccgacctg cccctggagg tggacttcgc 780

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cgaggagggg tggctattgg tggccctgga ctatagccag atagagctca gggtgctggc 960

ccacctctcc ggcgacgaga acctgatccg ggtcttccag gaggggcggg acatccacac 1020

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ccttcaggtc cacgacgagc tggtcctcga ggccccaaaa gagagggcgg aggccgtggc 1500

ccggctggcc aaggaggtca tggaggggtg gtatcccctg gccgtgcccc tggaggtgga 1560

ggtggggata ggggaggact ggctctccgc caaggagtga 1600

<210> 13

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 13
cacgaattcg gggatgctgc ccctctttga gcccaa 36

<210> 14

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 14
gtgagatcta tcactccttg gcggagagcc agtc 34

<210> 15

<211> 91

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 15
taatacgact cactataggg agaccggaat tcgagctcgc ccgggcgagc tcgaattccg 60

tgtattctat agtgtcacct aaatcgaatt c 91

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 16
taatacgact cactataggg 20

<210> 17

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 17
gaattcgatt taggtgacac tatagaa 27

<210> 18

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 18
gtaatcatgg tcatagctgg tagcttgcta c 31

<210> 19

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 19
ggatcctcta gagtcgacct gcaggcatgc ctaccttggt ag 42

<210> 20

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 20
ggatcctcta gagtcgacct gcaggcatgc 30

<210> 21

<211> 2502

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 21

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ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240

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gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480

gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600

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aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720

aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780

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gaggtgggga taggggagga ctggctctcc gccaaggagt ga 2502

<210> 22

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 22
gatttaggtg acactatag 19

<210> 23

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 23
acacaggtac cacatggtac aagaggcaag agagacgaca cagcagaaac 50

<210> 24

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 24

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser
1 5 10 15

<210> 25

<211> 969

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 25
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tttgagccca agggccgggt cctcctggtg gacggccacc acctggccta ccgcaccttc 120

cacgccctga agggcctcac caccagccgg ggggagccgg tgcaggcggt ctacggcttc 180

gccaagagcc tcctcaaggc cctcaaggag gacggggacg cggtgatcgt ggtctttgac 240

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acgccggagg actttccccg gcaactcgcc ctcatcaagg agctggtgga cctcctgggg 360

ctggcgcgcc tcgaggtccc gggctacgag gcggacgacg tcctggccag cctggccaag 420

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cttctttccg accgcatcca cgtcctccac cccgaggggt acctcatcac cccggcctgg 540

ctttgggaaa agtacggcct gaggcccgac cagtgggccg actaccgggc cctgaccggg 600

gacgagtccg acaaccttcc cggggtcaag ggcatcgggg agaagacggc gaggaagctt 660

ctggaggagt gggggagcct ggaagccctc ctcaagaacc tggaccggct gaagcccgcc 720

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ctggaaagcc ccaagtcatg gaggggtgt atcccctggc cgtgcccctg gaggtggagg 960

tggggatag 969

<210> 26

<211> 948

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 26

atggctagca tgactggtgg acagcaaatg ggtcggatca attcggggat gctgcccctc 60

tttgagccca agggccgggt cctcctggtg gacggccacc acctggccta ccgcaccttc 120

cacgccctga agggcctcac caccagccgg ggggagccgg tgcaggcggt ctacggcttc 180

gccaagagcc tcctcaaggc cctcaaggag gacggggacg cggtgatcgt ggtctttgac 240

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ctggaggagt gggggagcct ggaagccctc ctcaagaacc tggaccggct gaagcccgcc 720

atccgggaga agatcctggc ccacatggac gatctgaagc tctcctggga cctggccaag 780

gtgcgcaccg acctgccccc ggaggtggac ttcgccaaaa ggcgggagcc cgaccgggag 840

aggcttaggg cctttctgga gaggcttgag tttggcagcc tcctccacga gttcggcctt 900

ctggaaagcc ccaaggccgc actcgagcac caccaccacc accactga 948

<210> 27

<211> 206

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 27
cgccagggtt ttcccagtca cgacgttgta aaacgacggc cagtgaattg taatacgact 60

cactataggg cgaattcgag ctcggtaccc ggggatcctc tagagtcgac ctgcaggcat 120

gcaagcttga gtattctata gtgtcaccta aatagcttgg cgtaatcatg gtcatagctg 180

tttcctgtgt gaaattgtta tccgct 206

<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 28
aacagctatg accatgatta c 21

<210> 29

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 29
gttctctgct ctctggtcgc tgtctcgctt gtgaaacaag cgagacagcg tggtctctcg 60

<210> 30

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 30
cgagagacca cgctg 15

<210> 31

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 31
cctttcgctt tcttcccttc ctttctcgcc acgttcgccg gctttccccg tc 52

<210> 32

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 32
agaaaggaag ggaagaaagc gaaagg 26

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 33
gacggggaaa gccggcgaac g 21

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 34
gaaagccggc gaacgtggcg 20

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 35
ggcgaacgtg gcgagaaagg a 21

<210> 36

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 36
cctttcgctt tcttcccttc ctttctcgcc acgttcgccg gc 42

<210> 37

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 37
cctttcgctc tcttcccttc ctttctcgcc acgttcgccg gc 42

<210> 38

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (8)..(8)

<223> The residue at this position is 2'-O-methyladenosine.

<400> 38
agaaaggaag ggaagaaagc gaaaggt 27

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 39
gccggcgaac gtggcgagaa agga 24

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 40
ggtttttctt tgaggtttag 20

<210> 41

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 41
gcgacactcc accatagat 19

<210> 42

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 42
ctgtcttcac gcagaaagc 19

<210> 43

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 43
gcacggtcta cgagacctc 19

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 44
taatacgact cactataggg 20

<210> 45

<211> 337

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 45
gggaaagcuu gcaugccugc aggucgacuc uagaggaucu acuagucaua uggauucugu 60

cuucacgcag aaagcgucug gccauggcgu uaguaugagu gucgugcagc cuccaggacc 120

cccccucccg ggagaggcau aguggucugc ggaaccggug aguacaccgg aauugccagg 180

acgaccgggu ccuuucuugg auaaacccgc ucaaugccug gagauuuggg cgugcccccg 240

caagacugcu agccgaguag uguugggucg cgaaaggccu uguggguacug ccugauaggg 300

ugccugcgag ugccccggga ggucucguag accgugc 337

<210> 46

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (17)..(17)

<223> The T at this position is linked to a fluorescein dye on an abasi
c linker

<400> 46
ccggtcgtcc tggcaatcc 19

<210> 47

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 47
gtttatccaa gaaaggaccc ggtc 24

<210> 48

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 48
cagggtgaag ggaagaagaa agcgaaaggt 30

<210> 49

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 49
caggggggaag ggaagaagaa agcgaaaggt 30

<210> 50

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(2)

<223> The T residues at these positions are amino modified T residues.

<400> 50
ttcttttcac cagcgagacg gg 22

<210> 51

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 51
attgggcgcc agggtggttt tt 22

<210> 52

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 52
cccgtctcgc tggtgaaaag aaaaaccacc ctggcgccca atacgcaaac cgc 53

<210> 53

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 53
gaattcgatt taggtgacac tatagaatac a 31

<210> 54

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 54
cctttcgctt tcttcccttc ctttctcgcc acgttcgccg gc 42

<210> 55

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 55
gccggcgaac gtggcgagaa agga 24

<210> 56

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 56
cagaaggaag ggaagaaagc gaaagg 26

<210> 57

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 57
caggggaag ggaagaaagc gaaagg 26

<210> 58

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 58
cagggtacag ggaagaaagc gaaagg 26

<210> 59

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 59
gggaaagtcc tcggagccgc gcgggacgag cgtgggggcc cg 42

<210> 60

<211> 963

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1)..(960)

<400> 60

```
atg gct agc atg act ggt gga cag caa atg ggt cgg atc aat tcg ggg       48
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly
1               5                   10                  15

atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc ctg gtg gac ggc       96
Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
            20                  25                  30

cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag ggc ctc acc acc      144
His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
        35                  40                  45

agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc gcc aag agc ctc      192
Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
    50                  55                  60

ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc gtg gtc ttt gac      240
Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
65                  70                  75                  80

gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg ggg tac aag gcg      288
Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
                85                  90                  95

ggc cgg gcc ccc acg ctc gtc ccg cgc ggc tcc gag gac ttt ccc cgg      336
Gly Arg Ala Pro Thr Leu Val Pro Arg Gly Ser Glu Asp Phe Pro Arg
            100                 105                 110

caa ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc      384
Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg
        115                 120                 125

ctc gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc      432
Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala
    130                 135                 140

aag aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac      480
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
145                 150                 155                 160

aaa gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc      528
Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
                165                 170                 175

gag ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg      576
Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
            180                 185                 190

agg ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc      624
Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
        195                 200                 205

gac aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag      672
Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys
    210                 215                 220
```

```
ctt ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac      720
Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
225                 230                 235                 240

cgg ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat      768
Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
                245                 250                 255

ctg aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg      816
Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
            260                 265                 270

gag gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg      864
Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
        275                 280                 285

gcc ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc      912
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
    290                 295                 300

ctt ctg gaa agc ccc aag gcc gca ctc gag cac cac cac cac cac cac      960
Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His His
305                 310                 315                 320

tga                                                                  963
```

<210> 61

<211> 320

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 61

```
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly
1               5                   10                  15

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
            20                  25                  30

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
        35                  40                  45

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
    50                  55                  60

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
65                  70                  75                  80

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
```

85 90 95

Gly Arg Ala Pro Thr Leu Val Pro Arg Gly Ser Glu Asp Phe Pro Arg
100 105 110

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg
115 120 125

Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala
130 135 140

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
145 150 155 160

Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
165 170 175

Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
180 185 190

Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
195 200 205

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys
210 215 220

Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
225 230 235 240

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
245 250 255

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
260 265 270

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
275 280 285

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
290 295 300

Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His His
305 310 315 320

<210> 62

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 62
cgatctcctc ggccacctcc 20

<210> 63

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 63
ggcggtgccc tggacgggca 20

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 64
ccagctcgtt gtggacctga 20

<210> 65

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1)..(2499)

<400> 65

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atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc       48
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1               5                  10                  15

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag       96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
            20                  25                  30

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc      144
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
        35                  40                  45

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc      192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
    50                  55                  60

gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg      240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65                  70                  75                  80

ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa      288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
                85                  90                  95

ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc      336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
            100                 105                 110

gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag      384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
        115                 120                 125

aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa      432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
    130                 135                 140

gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag      480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145                 150                 155                 160

ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg      528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
                165                 170                 175

ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc gac      576
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
            180                 185                 190

aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt      624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
        195                 200                 205

ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg      672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
    210                 215                 220
```

```
ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg      720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225                 230                 235                 240

aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag      768
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
                245                 250                 255

gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc      816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
            260                 265                 270

ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt      864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
        275                 280                 285

ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa      912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
    290                 295                 300

ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc      960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305                 310                 315                 320

gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc     1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
                325                 330                 335

ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt     1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
            340                 345                 350

ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc     1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
        355                 360                 365

ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc     1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
    370                 375                 380

aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg     1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385                 390                 395                 400

gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac     1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
                405                 410                 415

ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg     1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
            420                 425                 430

gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg     1344
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
        435                 440                 445

ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg     1392
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
    450                 455                 460
```

```
gcc gag gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc      1440
Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465                 470                 475                 480

cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt      1488
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
                485                 490                 495

gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag      1536
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
            500                 505                 510

cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc      1584
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
        515                 520                 525

atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc      1632
Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
    530                 535                 540

acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc      1680
Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545                 550                 555                 560

ctc cac acc cgc ttc aac cag acg gcc acg gcc acg ggc agg cta agt      1728
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
                565                 570                 575

agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg      1776
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
            580                 585                 590

cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg      1824
Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
        595                 600                 605

gcc ctg gac tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc      1872
Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
    610                 615                 620

ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac      1920
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625                 630                 635                 640

acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac      1968
Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
                645                 650                 655

ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac      2016
Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
            660                 665                 670

ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag      2064
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
        675                 680                 685

gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg      2112
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
    690                 695                 700
```

```
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac      2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705                 710                 715                 720

gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc      2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
                725                 730                 735

cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg      2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
            740                 745                 750

ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag      2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
        755                 760                 765

ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc      2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
    770                 775                 780

cac aac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg      2400
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785                 790                 795                 800

gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg      2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
                805                 810                 815

ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag      2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
            820                 825                 830

gag tgatag                                                          2505
Glu
```

<210> 66

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 66

```
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1               5                   10                  15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
            20                  25                  30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
        35                  40                  45
```

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg

545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

<210> 67

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 67
tggctatagr ccagggccac 20

<210> 68

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1)..(2499)

<400> 68
atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc 48
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag 96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc 144
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc 192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

```
gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg      240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65                  70                  75                  80

ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa      288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
                85                  90                  95

ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc      336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
            100                 105                 110

gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag      384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
        115                 120                 125

aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa      432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
    130                 135                 140

gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag      480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145                 150                 155                 160

ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg      528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
                165                 170                 175

ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc gac      576
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
            180                 185                 190

aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt      624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
        195                 200                 205

ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg      672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
    210                 215                 220

ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg      720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225                 230                 235                 240

aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag      768
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
                245                 250                 255

gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc      816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
            260                 265                 270

ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt      864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
        275                 280                 285

ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa      912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
    290                 295                 300
```

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ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc      960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305                 310                 315                 320

gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc     1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
                325                 330                 335

ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt     1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
            340                 345                 350

ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc     1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
        355                 360                 365

ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc     1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
    370                 375                 380

aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg     1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385                 390                 395                 400

gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac     1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
                405                 410                 415

ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg     1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
            420                 425                 430

gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg     1344
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
        435                 440                 445

ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg     1392
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
    450                 455                 460

gcc ggg gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc     1440
Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465                 470                 475                 480

cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt     1488
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
                485                 490                 495

gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag     1536
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
            500                 505                 510

cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc     1584
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
        515                 520                 525
```

```
atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc      1632
Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
    530                 535                 540

acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc      1680
Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545                 550                 555                 560

ctc cac acc cgc ttc aac cag acg gcc acg gcc acg ggc agg cta agt      1728
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
                565                 570                 575

agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg      1776
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
            580                 585                 590

cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg      1824
Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
        595                 600                 605

gcc ctg gcc tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc      1872
Ala Leu Ala Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
    610                 615                 620

ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac      1920
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625                 630                 635                 640

acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac      1968
Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
                645                 650                 655

ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac      2016
Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
            660                 665                 670

ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag      2064
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
        675                 680                 685

gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg      2112
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
    690                 695                 700

cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac      2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705                 710                 715                 720

gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc      2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
                725                 730                 735

cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg      2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
            740                 745                 750

ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag      2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
        755                 760                 765
```

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ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc      2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
    770                 775                 780

cac gac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg      2400
His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785                 790                 795                 800

gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg      2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
                805                 810                 815

ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag      2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
            820                 825                 830

gag tgatag                                                          2505
Glu
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<210> 69

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 69

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Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1               5                   10                  15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
            20                  25                  30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
        35                  40                  45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
    50                  55                  60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65                  70                  75                  80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
                85                  90                  95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
            100                 105                 110
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Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Ala Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser

610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

<210> 70

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1)..(2499)

<400> 70

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Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1               5                  10                  15

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag       96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
            20                  25                  30

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc      144
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
        35                  40                  45

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc      192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
    50                  55                  60

gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg      240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65                  70                  75                  80

ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa      288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
                85                  90                  95

ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc      336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
            100                 105                 110

gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag      384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
        115                 120                 125

aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa      432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
    130                 135                 140

gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag      480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145                 150                 155                 160

ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg      528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
                165                 170                 175
```

```
ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc gac      576
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
            180                 185                 190

aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt      624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
        195                 200                 205

ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg      672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
    210                 215                 220

ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg      720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225                 230                 235                 240

aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag      768
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
                245                 250                 255

gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc      816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
            260                 265                 270

ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt      864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
        275                 280                 285

ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa      912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
    290                 295                 300

ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc      960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305                 310                 315                 320

gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc     1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
                325                 330                 335

ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt     1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
            340                 345                 350

ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc     1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
        355                 360                 365

ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc     1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
    370                 375                 380

aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg     1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385                 390                 395                 400

gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac     1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
                405                 410                 415
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ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg     1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
            420                 425                 430

gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg     1344
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
        435                 440                 445

ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg     1392
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
    450                 455                 460

gcc ggg gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc     1440
Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465                 470                 475                 480

cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt     1488
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
                485                 490                 495

gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag     1536
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
            500                 505                 510

cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc     1584
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
        515                 520                 525

atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc     1632
Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
    530                 535                 540

acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc     1680
Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545                 550                 555                 560

ctc cac acc cgc ttc aac cag acg gcc acg gcc acg ggc agg cta agt     1728
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
                565                 570                 575

agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg     1776
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
            580                 585                 590

cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg     1824
Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
        595                 600                 605

gcc ctg gtc tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc     1872
Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
    610                 615                 620

ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac     1920
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625                 630                 635                 640

acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac     1968
Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
                645                 650                 655

ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac     2016
Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
```

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            660                 665                 670

ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag     2064
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
        675                 680                 685

gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg     2112
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
    690                 695                 700

cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac     2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705                 710                 715                 720

gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc     2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
                725                 730                 735

cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg     2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
            740                 745                 750

ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag     2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
        755                 760                 765

ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc     2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
    770                 775                 780

cac gac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg     2400
His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785                 790                 795                 800

gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg     2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
                805                 810                 815

ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag     2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
            820                 825                 830

gag tgatag                                                         2505
Glu
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<210> 71

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 71

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met

740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

<210> 72

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 72
gggataccat gggagtgcag tttgg 25

<210> 73

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 73
ggtaaatttt tctcgtcgac atcccac 27

<210> 74

<211> 981

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1)..(978)

<400> 74

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atg gga gtg cag ttt ggt gat ttt att cca aaa aat att atc tcc ttt       48
Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
1               5                   10                  15

gaa gat tta aaa ggg aaa aaa gta gct att gat gga atg aat gca tta       96
Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
            20                  25                  30

tat cag ttt tta aca tct ata cgt ttg aga gat ggt tct cca ttg aga      144
Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
        35                  40                  45

aat aga aaa gga gag ata acc tca gca tat aac gga gtt ttt tat aaa      192
Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
    50                  55                  60

acc ata cat ttg tta gag aat gat ata act cca atc tgg gtt ttt gat      240
Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
65                  70                  75                  80

ggt gag cca cca aag tta aag gag aaa aca agg aaa gtt agg aga gag      288
Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
                85                  90                  95

atg aaa gag aaa gct gaa ctt aag atg aaa gag gca att aaa aag gag      336
Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
            100                 105                 110

gat ttt gaa gaa gct gct aag tat gca aag agg gtt agc tat cta act      384
Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
        115                 120                 125

ccg aaa atg gtt gaa aac tgc aaa tat ttg tta agt ttg atg ggc att      432
Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile
    130                 135                 140

ccg tat gtt gaa gct ccc tct gag gga gag gca caa gca agc tat atg      480
Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
145                 150                 155                 160

gca aag aag gga gat gtt tgg gca gtt gta agt caa gat tat gat gcc      528
Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
                165                 170                 175
```

```
ttg tta tat gga gct ccg aga gtt gtt aga aat tta aca act aca aag      576
Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
            180                 185                 190

gag atg cca gaa ctt att gaa tta aat gag gtt tta gag gat tta aga      624
Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
        195                 200                 205

att tct ttg gat gat ttg ata gat ata gcc ata ttt atg gga act gac      672
Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp
    210                 215                 220

tat aat cca gga gga gtt aaa gga ata gga ttt aaa agg gct tat gaa      720
Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu
225                 230                 235                 240

ttg gtt aga agt ggt gta gct aag gat gtt ttg aaa aaa gag gtt gaa      768
Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu
                245                 250                 255

tac tac gat gag att aag agg ata ttt aaa gag cca aag gtt acc gat      816
Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp
            260                 265                 270

aac tat tca tta agc cta aaa ttg cca gat aaa gag gga att ata aaa      864
Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys
        275                 280                 285

ttc tta gtt gat gaa aat gac ttt aat tat gat agg gtt aaa aag cat      912
Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His
    290                 295                 300

gtt gat aaa ctc tat aac tta att gca aac aaa act aag caa aaa aca      960
Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
305                 310                 315                 320

tta gat gca tgg ttt aaa taa                                         981
Leu Asp Ala Trp Phe Lys
                325
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<210> 75

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 75

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Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
1               5                   10                  15

Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
            20                  25                  30
```

```
Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
        35                  40                  45

Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
    50                  55                  60

Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
65                  70                  75                  80

Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
                85                  90                  95

Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
            100                 105                 110

Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
        115                 120                 125

Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile
    130                 135                 140

Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
145                 150                 155                 160

Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
                165                 170                 175

Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
            180                 185                 190

Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
        195                 200                 205

Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp
    210                 215                 220

Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu
225                 230                 235                 240

Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu
                245                 250                 255

Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp
            260                 265                 270

Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys
        275                 280                 285
```

Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His
290 295 300

Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
305 310 315 320

Leu Asp Ala Trp Phe Lys
325

<210> 76

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 76
gaggtgatac catgggtgtc c 21

<210> 77

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 77
gaaactctgc agcgcgtcag 20

<210> 78

<211> 1023

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1)..(1020)

<400> 78

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atg ggt gtc cca att ggt gag att ata cca aga aaa gaa att gag tta       48
Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
1               5                  10                  15

gaa aac cta tac ggg aaa aaa atc gca atc gac gct ctt aat gca atc       96
Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
            20                  25                  30

tac caa ttt ttg tcc aca ata aga cag aaa gat gga act cca ctt atg      144
Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
        35                  40                  45

gat tca aag ggt aga ata acc tcc cac cta agc ggg ctc ttt tac agg      192
Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
    50                  55                  60

aca ata aac cta atg gag gct gga ata aaa cct gtg tat gtt ttt gat      240
Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
65                  70                  75                  80

gga gaa cct cca gaa ttc aaa aag aaa gag ctc gaa aaa aga aga gaa      288
Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
                85                  90                  95

gcg aga gag gaa gct gaa gaa aag tgg aga gaa gca ctt gaa aaa gga      336
Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly
            100                 105                 110

gag ata gag gaa gca aga aaa tat gcc caa aga gca acc agg gta aat      384
Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn
        115                 120                 125

gaa atg ctc atc gag gat gca aaa aaa ctc tta gag ctt atg gga att      432
Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile
    130                 135                 140

cct ata gtt caa gca cct agc gag gga gag gcc caa gct gca tat atg      480
Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met
145                 150                 155                 160

gcc gca aag ggg agc gtg tat gca tcg gct agt caa gat tac gat tcc      528
Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser
                165                 170                 175

cta ctt ttt gga gct cca aga ctt gtt aga aac tta aca ata aca gga      576
Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly
            180                 185                 190

aaa aga aag ttg cct ggg aaa aat gtc tac gtc gag ata aag ccc gag      624
Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu
        195                 200                 205

ttg ata att ttg gag gaa gta ctc aag gaa tta aag cta aca aga gaa      672
Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
    210                 215                 220

aag ctc att gaa cta gca atc ctc gtt gga aca gac tac aac cca gga      720
```

```
Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
225                 230                 235                 240

gga ata aag ggc ata ggc ctt aaa aaa gct tta gag att gtt aga cac      768
Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
                245                 250                 255

tca aaa gat ccg cta gca aag ttc caa aag caa agc gat gtg gat tta      816
Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
            260                 265                 270

tat gca ata aaa gag ttc ttc cta aac cca cca gtc aca gat aac tac      864
Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
        275                 280                 285

aat tta gtg tgg aga gat ccc gac gaa gag gga ata cta aag ttc tta      912
Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
    290                 295                 300

tgt gac gag cat gac ttt agt gag gaa aga gta aag aat gga tta gag      960
Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
305                 310                 315                 320

agg ctt aag aag gca atc aaa agt gga aaa caa tca acc ctt gaa agt     1008
Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
                325                 330                 335

tgg ttc aag aga taa                                                1023
Trp Phe Lys Arg
            340
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<210> 79

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 79

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Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
1               5                   10                  15

Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
            20                  25                  30

Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
        35                  40                  45

Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
    50                  55                  60
```

Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
85 90 95

Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly
100 105 110

Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn
115 120 125

Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile
130 135 140

Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met
145 150 155 160

Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser
165 170 175

Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly
180 185 190

Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu
195 200 205

Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
210 215 220

Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
225 230 235 240

Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
245 250 255

Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
260 265 270

Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
275 280 285

Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
290 295 300

Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
305 310 315 320

Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
325 330 335

Trp Phe Lys Arg
340

<210> 80

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 80
gataccatgg gtgtcccaat tggtg 25

<210> 81

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 81
tcgacgtcga cttatctctt gaaccaactt tcaaggg 37

<210> 82

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 82
agcgagggag aggcccaagc 20

<210> 83

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 83
gcctatgccc tttattcctc c 21

<210> 84

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 84
tggtcgctgt ctcgctgaaa gcgagacagc gtg 33

<210> 85

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 85
tgctctctgg tcgctgtctg aaagacagcg 30

<210> 86

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> The residue at this position is linked to a spacer containing a f
luorescein label

<400> 86
agaaaggaag ggaagaaagc gaaagg 26

<210> 87

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (26)..(26)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<220>

<221> modified_base

<222> (27)..(27)

<223> The residue at this position is a dideoxycytidine.

<400> 87
agaaaggaag ggaagaaagc gaaaggc 27

<210> 88

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (24)..(24)

<223> The residue at this position is a dideoxycytidine.

<400> 88
gccggcgaac gtggcgagaa aggc 24

<210> 89

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> The residue at this position is linked to a spacer containing a f luorescein label

<220>

<221> misc_feature

<222> (26)..(26)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<220>

<221> modified_base

<222> (27)..(27)

<223> The residue at this position is a dideoxycytidine.

<400> 89
agaaaggaag ggaagaaagc gaaaggc 27

<210> 90

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 90
aaaattcctt tctctttgcc ctttgcttcc 30

<210> 91

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 91
ggaaagccgg cgaacgtggc gagaaa 26

<210> 92

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 92
ggaaagccgg cgaacgtggc gaga 24

<210> 93

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> The residue at this position is linked to a spacer containing Cy3

<220>

<221> misc_feature

<222> (26)..(26)

<223> The residue at this position is linked to a spacer containing a f
luorescein label

<400> 93
agaaaggaag ggaagaaagc gaaaggt 27

<210> 94

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> The residue at this position is linked to a spacer containing Cy3

<220>

<221> modified_base

<222> (1)..(2)

<223> The residues at these positions are amine-T.

<220>

<221> misc_feature

<222> (22)..(22)

<223> The residue at this position is linked to a spacer containing a f luorescein label

<400> 94
ttccagagcc taatttgcca gta 23

<210> 95

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(1)

<223> The residue at this position has a 5' TET-label.

<220>

<221> misc_feature

<222> (22)..(22)

<400> 95
ttccagagcc taatttgcca gta 23

<210> 96

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 96
cttaccaacg ctaacgagcg tcttg 25

<210> 97

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 97
cccgtctcgc tggtgaaaag aaaaaccacc ctggcgccca ata 43

<210> 98

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 98
tattgggcgc catggtggtt ttt 23

<210> 99

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (10)..(10)

<223> The residue at this position is a 5-nitroindole.

<220>

<221> misc_difference

<222> (16)..(16)

<223> The residue at this position is a 5-nitroindole.

<400> 99
tattgggcgn cagggnggtt ttt 23

<210> 100

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (10)..(10)

<223> The residue at this position is a 5-nitroindole.

<220>

<221> misc_difference

<222> (16)..(16)

<223> The residue at this position is a 5-nitroindole.

<400> 100
tattgggcgn catggnggtt ttt 23

<210> 101

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (16)..(16)

<223> The residue at this position is a 3-nitropyrrole group.

<400> 101
tattgggcgc cagggnggtt ttt 23

<210> 102

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (16)..(16)

<223> The residue at this position is a 3-nitropyrrole group.

<400> 102
tattgggcgc catggnggtt ttt 23

<210> 103

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon ophosphate)

<220>

<221> misc_difference

<222> (2)..(2)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (3)..(3)

<223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (4)..(5)

<223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th iomonophosphate)

<220>

<221> misc_difference

<222> (6)..(6)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (7)..(7)

<223> The residue at this position is a 2'deoxyadenosine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (8)..(8)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (9)..(10)

<223> The residue at these positions are a 2'deoxyadenosine 5'-O-(1-Thi
omonophosphate)

<400> 103
ctgaatataa acttgtggta gttggagctg gtgccgtagg caagagtgcc ttgacg 56

<210> 104

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon
ophosphate)

<220>

<221> misc_difference

<222> (2)..(2)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
nophosphate)

<220>

<221> misc_difference

<222> (3)..(3)

<223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo
nophosphate)

<220>

<221> misc_difference

<222> (4)..(5)

<223> The residue at these positions are a 2'deoxyadenosine 5'-O-(1-Thi
omonophosphate)

<220>

<221> misc_difference

<222> (6)..(6)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (7)..(7)

<223> The residue at this position is a 2'deoxyadenosine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (8)..(8)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (9)..(10)

<223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th iomonophosphate)

<400> 104
ctgaatataa acttgtggta gttggagctg gtgacgtagg caagagtgcc ttgacg 56

<210> 105

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (2)..(2)

<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon ophosphate)

<220>

<221> misc_difference

<222> (3)..(3)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (4)..(4)

<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon ophosphate)

<220>

<221> misc_difference

<222> (5)..(6)

<223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th iomonophosphate)

<220>

<221> misc_difference

<222> (7)..(8)

<223> The residues at these positions are a 2'deoxyguanosine 5'-O-(1-Th iomonophosphate)

<220>

<221> misc_difference

<222> (9)..(9)

<223> The residues at this position is a 2'deoxycytosine 5'-O-(1-Thiomo nophosphate)

<400> 105
gctcaaggca ctcttgccta cga 23

<210> 106

<211> 8

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position is linked to a spacer bearing a Cy3 amidite label

<220>

<221> modified_base

<222> (1)..(2)

<223> The residues at these positions have an amino group added.

<400> 106
ttcaccag 8

<210> 107

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon ophosphate)

<220>

<221> misc_difference

<222> (2)..(2)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (3)..(4)

<223> The residues at these positions are a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc_difference

<222> (5)..(6)

<223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc_difference

<222> (7)..(7)

<223> The residues at these positions are a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc_difference

<222> (8)..(8)

<223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc_difference

<222> (9)..(9)

<223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)

<400> 107
ctccaactac cacaagttta tattcag 27

<210> 108

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 108
cgagagacca cgct 14

<210> 109

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (14)..(14)

<223> The residue at this position contains an abasic ribose.

<400> 109
cgagagacca cgct 14

<210> 110

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (14)..(14)

<223> The residue at this position contains an abasic ribose with a 3' phosphate group

<400> 110
cgagagacca cgct 14

<210> 111

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (15)..(15)

<223> The residue at this position contains a 3' phosphate group.

<400> 111
cgagagacca cgctg 15

<210> 112

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc_difference

<222> (2)..(2)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc_difference

<222> (3)..(4)

<223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc_difference

<222> (5)..(5)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc_difference

<222> (6)..(6)

<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon ophosphate)

<220>

<221> misc_difference

<222> (7)..(8)

<223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Th iomonophosphate)

<220>

<221> misc_difference

<222> (9)..(9)

<223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th iomonophosphate)

<220>

<221> misc_difference

<222> (10)..(10)

<223> The residues at these positions are a 2'deoxycytosine 5'-O-(1-Thi omonophosphate)

<400> 112
gtaatcttac caacgctaac gagcgtcttg 30

<210> 113

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(2)

<223> The residues at these positions are a 2'deoxycytosine 5'-O-(1-Thi omonophosphate)

<220>

<221> misc_difference

<222> (3)..(3)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (4)..(5)

<223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th iomonophosphate)

<220>

<221> misc_difference

<222> (6)..(8)

<223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Th iomonophosphate)

<220>

<221> misc_difference

<222> (9)..(9)

<223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo nophosphate)

<220>

<221> misc_difference

<222> (10)..(10)

<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon ophosphate)

<400> 113
cctaatttgc cagttacaaa ataaacagcc c 31

<210> 114

<211> 8

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<220>

<221> modified_base

<222> (1)..(2)

<223> The residues at these positions have an amino group added.

<400> 114
ttccagag 8

<210> 115

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 115
ttttccagag cctaatgaaa ttaggctctg gaaagacgct cgtg 44

<210> 116

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 116
aacgagcgtc tttg 14

<210> 117

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 117
aacgagcgtc attg 14

<210> 118

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 118
ttttttttta attaggctct ggaaagacgc tcgtgaaacg agcgtctttg 50

<210> 119

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 119
ttttccagag cctaatg 17

<210> 120

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position has a TET label.

<400> 120
ccggtcgtcc tgg 13

<210> 121

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 121
caattccggt gtactcaccg gttcc 25

<210> 122

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position has a TET label.

<400> 122
ccggtcgtcc tggcaa 16

<210> 123

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 123
tgttttgacc tccatagaag accctatagt gagtcgtatt aatttcg 47

<210> 124

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 124
cgaaattaat acgactcact ata 23

<210> 125

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 125
cgaaattaat acgactcact atacccagaa 30

<210> 126

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 126
cgaaattaat acgact 16

<210> 127

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 127
cgaaattaat acg 13

<210> 128

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 128
cgaaattaat ac 12

<210> 129

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 129
cactataggg tcttctatgg aggtc 25

<210> 130

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 130
actcactata gggtcttcta tggaggtc 28

<210> 131

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 131
gactcactat agggtcttct atggaggtc 29

<210> 132

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 132
cgaaattaat acgcagtatg ttagcaaacg 30

<210> 133

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 133
gaactggcat gattaagact ccttattacc 30

<210> 134

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 134
gaactggcat gattaagact ccttattaa 29

<210> 135

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 135

Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
1 5 10 15

Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
20 25 30

Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
35 40 45

Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
50 55 60

Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
85 90 95

Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
100 105 110

Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
115 120 125

Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile
130 135 140

Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
145 150 155 160

Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
165 170 175

Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
180 185 190

Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
195 200 205

Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp
210 215 220

Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu
225 230 235 240

Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu
245 250 255

Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp
260 265 270

Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys
275 280 285

Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His
290 295 300

Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
305 310 315 320

Leu Asp Ala Trp Phe Lys
325

<210> 136

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 136

Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
1 5 10 15

Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
20 25 30

Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
35 40 45

Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
50 55 60

Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
85 90 95

Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly
100 105 110

Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn
115 120 125

Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile
130 135 140

Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met
145 150 155 160

Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser
165 170 175

Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly
180 185 190

Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu
195 200 205

Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
210 215 220

Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
225 230 235 240

Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
245 250 255

Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
260 265 270

Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
275 280 285

Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
290 295 300

Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
305 310 315 320

Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
325 330 335

Trp Phe Lys Arg
340

<210> 137

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 137

Met Gly Ile Gln Gly Leu Ala Lys Leu Ile Ala Asp Val Ala Pro Ser
1 5 10 15

Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
20 25 30

Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
35 40 45

Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
50 55 60

Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
65 70 75 80

Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu
85 90 95

Leu Ala Lys Arg Ser Glu Arg Arg Ala Glu Ala Glu Lys Gln Leu Gln
100 105 110

Gln Ala Gln Ala Ala Gly Ala Glu Gln Glu Val Glu Lys Phe Thr Lys
115 120 125

Arg Leu Val Lys Val Thr Lys Gln His Asn Asp Glu Cys Lys His Leu
130 135 140

Leu Ser Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu
145 150 155 160

Ala Ser Cys Ala Ala Leu Val Lys Ala Gly Lys Val Tyr Ala Ala Ala
165 170 175

Thr Glu Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg
180 185 190

His Leu Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His
195 200 205

Leu Ser Arg Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val
210 215 220

Asp Leu Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly
225 230 235 240

Ile Gly Pro Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys Ser Ile
245 250 255

Glu Glu Ile Val Arg Arg Leu Asp Pro Asn Lys Tyr Pro Val Pro Glu
260 265 270

Asn Trp Leu His Lys Glu Ala His Gln Leu Phe Leu Glu Pro Glu Val
275 280 285

Leu Asp Pro Glu Ser Val Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu
290 295 300

Glu Leu Ile Lys Phe Met Cys Gly Glu Lys Gln Phe Ser Glu Glu Arg
305 310 315 320

Ile Arg Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr
325 330 335

Gln Gly Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser
340 345 350

Ala Lys Arg Lys Glu Pro Glu Pro Lys Gly Ser Thr Lys Lys Lys Ala
355 360 365

Lys Thr Gly Ala Ala Gly Lys Phe Lys Arg Gly Lys
370 375 380

<210> 138

<211> 378

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 138

Met Gly Ile His Gly Leu Ala Lys Leu Ile Ala Asp Val Ala Pro Ser
1 5 10 15

Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
20 25 30

Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
35 40 45

Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser Leu Met
50 55 60

Gly Met Phe Tyr Arg Thr Ile Arg Met Glu Asn Gly Ile Lys Pro Val
65 70 75 80

Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu Leu Ala
85 90 95

Lys Arg Ser Glu Arg Arg Ala Glu Ala Glu Lys Gln Leu Gln Gln Ala
100 105 110

Gln Glu Ala Gly Met Glu Glu Glu Val Glu Lys Phe Thr Lys Arg Leu
115 120 125

Val Lys Val Thr Lys Gln His Asn Asp Glu Cys Lys His Leu Leu Ser
130 135 140

Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu Ala Ser
145 150 155 160

Cys Ala Ala Leu Ala Lys Ala Gly Lys Val Tyr Ala Ala Ala Thr Glu
165 170 175

Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg His Leu
180 185 190

Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His Leu Ser
195 200 205

Arg Val Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val Asp Leu
210 215 220

Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly Ile Gly
225 230 235 240

Ala Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys Ser Ile Glu Glu
245 250 255

Ile Val Arg Arg Leu Asp Pro Ser Lys Tyr Pro Val Pro Glu Asn Trp
260 265 270

Leu His Lys Glu Ala Gln Gln Leu Phe Leu Glu Pro Glu Val Val Asp
275 280 285

Pro Glu Ser Val Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu Glu Leu
290 295 300

Val Lys Phe Met Cys Gly Glu Lys Gln Phe Ser Glu Glu Arg Ile Arg
305 310 315 320

Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr Gln Gly
325 330 335

Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser Ala Lys
340 345 350

Arg Lys Glu Pro Glu Pro Lys Gly Pro Ala Lys Lys Lys Ala Lys Thr
355 360 365

Gly Gly Ala Gly Lys Phe Arg Arg Gly Lys
370 375

<210> 139

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 139

Met Gly Ile Lys Gly Leu Asn Ala Ile Ile Ser Glu His Val Pro Ser
1 5 10 15

Ala Ile Arg Lys Ser Asp Ile Lys Ser Phe Phe Gly Arg Lys Val Ala
20 25 30

Ile Asp Ala Ser Met Ser Leu Tyr Gln Phe Leu Ile Ala Val Arg Gln
35 40 45

Gln Asp Gly Gly Gln Leu Thr Asn Glu Ala Gly Glu Thr Thr Ser His
50 55 60

Leu Met Gly Met Phe Tyr Arg Thr Leu Arg Met Ile Asp Asn Gly Ile
65 70 75 80

Lys Pro Cys Tyr Val Phe Asp Gly Lys Pro Pro Asp Leu Lys Ser His
85 90 95

Glu Leu Thr Lys Arg Ser Ser Arg Arg Val Glu Thr Glu Lys Lys Leu
100 105 110

Ala Glu Ala Thr Thr Glu Leu Glu Lys Met Lys Gln Glu Arg Arg Leu
115 120 125

Val Lys Val Ser Lys Glu His Asn Glu Glu Ala Gln Lys Leu Leu Gly
130 135 140

Leu Met Gly Ile Pro Tyr Ile Ile Ala Pro Thr Glu Ala Glu Ala Gln
145 150 155 160

Cys Ala Glu Leu Ala Lys Lys Gly Lys Val Tyr Ala Ala Ala Ser Glu
165 170 175

Asp Met Asp Thr Leu Cys Tyr Arg Thr Pro Phe Leu Leu Arg His Leu
180 185 190

Thr Phe Ser Glu Ala Lys Lys Glu Pro Ile His Glu Ile Asp Thr Glu
195 200 205

Leu Val Leu Arg Gly Leu Asp Leu Thr Ile Glu Gln Phe Val Asp Leu
210 215 220

Cys Ile Met Leu Gly Cys Asp Tyr Cys Glu Ser Ile Arg Gly Val Gly
225 230 235 240

Pro Val Thr Ala Leu Lys Leu Ile Lys Thr His Gly Ser Ile Glu Lys
245 250 255

Ile Val Glu Phe Ile Glu Ser Gly Glu Ser Asn Asn Thr Lys Trp Lys
260 265 270

Ile Pro Glu Asp Trp Pro Tyr Lys Gln Ala Arg Met Leu Phe Leu Asp
275 280 285

Pro Glu Val Ile Asp Gly Asn Glu Ile Asn Leu Lys Trp Ser Pro Pro
290 295 300

Lys Glu Lys Glu Leu Ile Glu Tyr Leu Cys Asp Asp Lys Lys Phe Ser
305 310 315 320

Glu Glu Arg Val Lys Ser Gly Ile Ser Arg Leu Lys Lys Gly Leu Lys
325 330 335

Ser Gly Ile Gln Gly Arg Leu Asp Gly Phe Phe Gln Val Val Pro Lys
340 345 350

Thr Lys Glu Gln Leu Ala Ala Ala Ala Lys Arg Ala Gln Glu Asn Lys
355 360 365

Lys Leu Asn Lys Asn Lys Asn Lys Val Thr Lys Gly Arg Arg
370 375 380

<210> 140

<211> 387

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 140

Met Gly Val His Ser Phe Trp Asp Ile Ala Gly Pro Thr Ala Arg Pro
1 5 10 15

Val Arg Leu Glu Ser Leu Glu Asp Lys Arg Met Ala Val Asp Ala Ser
20 25 30

Ile Trp Ile Tyr Gln Phe Leu Lys Ala Val Arg Asp Gln Glu Gly Asn
35 40 45

Ala Val Lys Asn Ser His Ile Thr Gly Phe Phe Arg Arg Ile Cys Lys
50 55 60

Leu Leu Tyr Phe Gly Ile Arg Pro Val Phe Val Phe Asp Gly Gly Val
65 70 75 80

Pro Val Leu Lys Arg Glu Thr Ile Arg Gln Arg Lys Glu Arg Arg Gln
85 90 95

Gly Lys Arg Glu Ser Ala Lys Ser Thr Ala Arg Lys Leu Leu Ala Leu
100 105 110

Gln Leu Gln Asn Gly Ser Asn Asp Asn Glu Val Thr Met Asp Met Ile
115 120 125

Lys Glu Val Gln Glu Leu Leu Ser Arg Phe Gly Ile Pro Tyr Ile Thr
130 135 140

Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Glu Leu Leu Gln Leu Asn
145 150 155 160

Leu Val Asp Gly Ile Ile Thr Asp Asp Ser Asp Val Phe Leu Phe Gly
165 170 175

Gly Thr Lys Ile Tyr Lys Asn Met Phe His Glu Lys Asn Tyr Val Glu
180 185 190

Phe Tyr Asp Ala Glu Ser Ile Leu Lys Leu Leu Gly Leu Asp Arg Lys
195 200 205

Asn Met Ile Glu Leu Ala Gln Leu Leu Gly Ser Asp Tyr Thr Asn Gly
210 215 220

Leu Lys Gly Met Gly Pro Val Ser Ser Ile Glu Val Ile Ala Glu Phe
225 230 235 240

Gly Asn Leu Lys Asn Phe Lys Asp Trp Tyr Asn Asn Gly Gln Phe Asp
245 250 255

Lys Arg Lys Gln Glu Thr Glu Asn Lys Phe Glu Lys Asp Leu Arg Lys
260 265 270

Lys Leu Val Asn Asn Glu Ile Ile Leu Asp Asp Asp Phe Pro Ser Val
275 280 285

Met Val Tyr Asp Ala Tyr Met Arg Pro Glu Val Asp His Asp Thr Thr
290 295 300

Pro Phe Val Trp Gly Val Pro Asp Leu Asp Met Leu Arg Ser Phe Met
305 310 315 320

Lys Thr Gln Leu Gly Trp Pro His Glu Lys Ser Asp Glu Ile Leu Ile
325 330 335

Pro Leu Ile Arg Asp Val Asn Lys Arg Lys Lys Lys Gly Lys Gln Lys
340 345 350

Arg Ile Asn Glu Phe Phe Pro Arg Glu Tyr Ile Ser Gly Asp Lys Lys
355 360 365

Leu Asn Thr Ser Lys Arg Ile Ser Thr Ala Thr Gly Lys Leu Lys Lys
370 375 380

Arg Lys Met
385

<210> 141

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 141

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Met Gly Val Ser Gly Leu Trp Asn Ile Leu Glu Pro Val Lys Arg Pro
1               5                  10                  15

Val Lys Leu Glu Thr Leu Val Asn Lys Arg Leu Ala Ile Asp Ala Ser
            20                  25                  30

Ile Trp Ile Tyr Gln Phe Leu Lys Ala Val Arg Asp Lys Glu Gly Asn
        35                  40                  45

Gln Leu Lys Ser Ser His Val Val Gly Phe Phe Arg Arg Ile Cys Lys
    50                  55                  60

Leu Leu Phe Phe Gly Ile Lys Pro Val Phe Val Phe Asp Gly Gly Ala
65                  70                  75                  80

Pro Ser Leu Lys Arg Gln Thr Ile Gln Lys Arg Gln Ala Arg Arg Leu
                85                  90                  95

Asp Arg Glu Glu Asn Ala Thr Val Thr Ala Asn Lys Leu Leu Ala Leu
            100                 105                 110

Gln Met Arg His Gln Ala Met Leu Leu Lys Arg Asp Ala Asp Glu Val
        115                 120                 125

Thr Gln Val Met Ile Lys Glu Cys Gln Glu Leu Leu Arg Leu Phe Gly
    130                 135                 140

Leu Pro Tyr Ile Val Ala Pro Gln Glu Ala Glu Ala Gln Cys Ser Lys
145                 150                 155                 160

Leu Leu Glu Leu Lys Leu Val Asp Gly Ile Val Thr Asp Asp Ser Asp
                165                 170                 175

Val Phe Leu Phe Gly Gly Thr Arg Val Tyr Arg Asn Met Phe Asn Gln
            180                 185                 190

Asn Lys Phe Val Glu Leu Tyr Leu Met Asp Asp Met Lys Arg Glu Phe
        195                 200                 205

Asn Val Asn Gln Met Asp Leu Ile Lys Leu Ala His Leu Leu Gly Ser
    210                 215                 220

Asp Tyr Thr Met Gly Leu Ser Arg Val Gly Pro Val Leu Ala Leu Glu
225                 230                 235                 240

Ile Leu His Glu Phe Pro Gly Asp Thr Gly Leu Phe Glu Phe Lys Lys
                245                 250                 255
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Trp Phe Gln Arg Leu Ser Thr Gly His Ala Ser Lys Asn Asp Val Asn
260 265 270

Thr Pro Val Lys Lys Arg Ile Asn Lys Leu Val Gly Lys Ile Ile Leu
275 280 285

Pro Ser Glu Phe Pro Asn Pro Leu Val Asp Glu Ala Tyr Leu His Pro
290 295 300

Ala Val Asp Asp Ser Lys Gln Ser Phe Gln Trp Gly Ile Pro Asp Leu
305 310 315 320

Asp Glu Leu Arg Gln Phe Leu Met Ala Thr Val Gly Trp Ser Lys Gln
325 330 335

Arg Thr Asn Glu Val Leu Leu Pro Val Ile Gln Asp Met His Lys Lys
340 345 350

Gln Phe Val Gly Thr Gln Ser Asn Leu Thr Gln Phe Phe Glu Gly Gly
355 360 365

Asn Thr Asn Val Tyr Ala Pro Arg Val Ala Tyr His Phe Lys Ser Lys
370 375 380

Arg Leu Glu Asn Ala Leu Ser Ser Phe Lys Asn Gln Ile Ser Asn Gln
385 390 395 400

Ser Pro Met Ser Glu Glu Ile Gln Ala Asp Ala Asp Ala Phe Gly Glu
405 410 415

Ser Lys Gly Ser Asp Glu Leu Gln Ser Arg Ile Leu Arg Arg Lys Lys
420 425 430

Met Met Ala Ser Lys Asn Ser Ser Asp Ser Asp Ser Asp Ser Glu Asp
435 440 445

Asn Phe Leu Ala Ser Leu Thr Pro Lys Thr Asn Ser Ser Ser Ile Ser
450 455 460

Ile Glu Asn Leu Pro Arg Lys Thr Lys Leu Ser Thr Ser Leu Leu Lys
465 470 475 480

Lys Pro Ser Lys Arg Arg Arg Lys
485

<210> 142

<211> 550

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 142

Met Gly Val Gln Gly Leu Trp Lys Leu Leu Glu Cys Ser Gly Arg Gln
1 5 10 15

Val Ser Pro Glu Ala Leu Glu Gly Lys Ile Leu Ala Val Asp Ile Ser
20 25 30

Ile Trp Leu Asn Gln Ala Leu Lys Gly Val Arg Asp Arg His Gly Asn
35 40 45

Ser Ile Glu Asn Pro His Leu Leu Thr Leu Phe His Arg Leu Cys Lys
50 55 60

Leu Leu Phe Phe Arg Ile Arg Pro Ile Phe Val Phe Asp Gly Asp Ala
65 70 75 80

Pro Leu Leu Lys Lys Gln Thr Leu Val Lys Arg Arg Gln Arg Lys Asp
85 90 95

Leu Ala Ser Ser Asp Ser Arg Lys Thr Thr Glu Lys Leu Leu Lys Thr
100 105 110

Phe Leu Lys Arg Gln Ala Ile Lys Thr Glu Arg Ile Ala Ala Thr Val
115 120 125

Thr Gly Gln Met Phe Leu Glu Ser Gln Glu Leu Leu Arg Leu Phe Gly
130 135 140

Ile Pro Tyr Ile Gln Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Ile
145 150 155 160

Leu Asp Leu Thr Asp Gln Thr Ser Gly Thr Ile Thr Asp Asp Ser Asp
165 170 175

Ile Trp Leu Phe Gly Ala Arg His Val Tyr Arg Asn Phe Phe Asn Lys
180 185 190

Asn Lys Phe Val Glu Tyr Tyr Gln Tyr Val Asp Phe His Asn Gln Leu
195 200 205

Gly Leu Asp Arg Asn Lys Leu Ile Asn Leu Ala Tyr Leu Leu Gly Ser
210 215 220

Asp Tyr Thr Glu Gly Ile Pro Thr Val Gly Cys Val Thr Ala Met Glu
225 230 235 240

Ile Leu Asn Glu Phe Pro Gly His Gly Leu Glu Pro Leu Leu Lys Phe
245 250 255

Ser Glu Trp Trp His Glu Ala Gln Lys Asn Pro Lys Ile Arg Pro Asn
260 265 270

Pro His Asp Thr Lys Val Lys Lys Lys Leu Arg Thr Leu Gln Leu Thr
275 280 285

Pro Gly Phe Pro Asn Pro Ala Val Ala Glu Ala Tyr Leu Lys Pro Val
290 295 300

Val Asp Asp Ser Lys Gly Ser Phe Leu Trp Gly Lys Pro Asp Leu Asp
305 310 315 320

Lys Ile Arg Glu Phe Cys Gln Arg Tyr Phe Gly Trp Asn Arg Thr Lys
325 330 335

Thr Asp Glu Ser Leu Phe Pro Val Leu Lys Gln Leu Asp Ala Gln Gln
340 345 350

Thr Gln Leu Arg Ile Asp Ser Phe Phe Arg Leu Ala Gln Gln Glu Lys
355 360 365

Glu Asp Ala Lys Arg Ile Lys Ser Gln Arg Leu Asn Arg Ala Val Thr
370 375 380

Cys Met Leu Arg Lys Glu Lys Glu Ala Ala Ala Ser Glu Ile Glu Ala
385 390 395 400

Val Ser Val Ala Met Glu Lys Glu Phe Glu Leu Leu Asp Lys Ala Lys
405 410 415

Arg Lys Thr Gln Lys Arg Gly Ile Thr Asn Thr Leu Glu Glu Ser Ser
420 425 430

Ser Leu Lys Arg Lys Arg Leu Ser Asp Ser Lys Arg Lys Asn Thr Cys
435 440 445

Gly Gly Phe Leu Gly Glu Thr Cys Leu Ser Glu Ser Ser Asp Gly Ser
450 455 460

Ser Ser Glu His Ala Glu Ser Ser Ser Leu Met Asn Val Gln Arg Arg
465 470 475 480

Thr Ala Ala Lys Glu Pro Lys Thr Ser Ala Ser Asp Ser Gln Asn Ser
485 490 495

Val Lys Glu Ala Pro Val Lys Asn Gly Gly Ala Thr Thr Ser Ser Ser
500 505 510

Ser Asp Ser Asp Asp Asp Gly Gly Lys Glu Lys Met Val Leu Val Thr
515 520 525

Ala Arg Ser Val Phe Gly Lys Lys Arg Arg Lys Leu Arg Arg Ala Arg
530 535 540

Gly Arg Lys Arg Lys Thr
545 550

<210> 143

<211> 543

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 143

Met Gly Val Gln Gly Leu Trp Lys Leu Leu Glu Cys Ser Gly His Arg
1 5 10 15

Val Ser Pro Glu Ala Leu Glu Gly Lys Val Leu Ala Val Asp Ile Ser
20 25 30

Ile Trp Leu Asn Gln Ala Leu Lys Gly Val Arg Asp Ser His Gly Asn
35 40 45

Val Ile Glu Asn Ala His Leu Leu Thr Leu Phe His Arg Leu Cys Lys
50 55 60

Leu Leu Phe Phe Arg Ile Arg Pro Ile Phe Val Phe Asp Gly Asp Ala
65 70 75 80

Pro Leu Leu Lys Lys Gln Thr Leu Ala Lys Arg Arg Gln Arg Lys Asp
85 90 95

Ser Ala Ser Ile Asp Ser Arg Lys Thr Thr Glu Lys Leu Leu Lys Thr
100 105 110

Phe Leu Lys Arg Gln Ala Leu Lys Thr Asp Arg Ile Ala Ala Ser Val
115 120 125

Thr Gly Gln Met Phe Leu Glu Ser Gln Glu Leu Leu Arg Leu Phe Gly
130 135 140

Val Pro Tyr Ile Gln Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Val
145 150 155 160

Leu Asp Leu Ser Asp Gln Thr Ser Gly Thr Ile Thr Asp Asp Ser Asp
165 170 175

Ile Trp Leu Phe Gly Ala Arg His Val Tyr Lys Asn Phe Phe Asn Lys
180 185 190

Asn Lys Phe Val Glu Tyr Tyr Gln Tyr Val Asp Phe Tyr Ser Gln Leu
195 200 205

Gly Leu Asp Arg Asn Lys Leu Ile Asn Leu Ala Tyr Leu Leu Gly Ser
210 215 220

Asp Tyr Thr Glu Gly Ile Pro Thr Val Gly Cys Val Thr Ala Met Glu
225 230 235 240

Ile Leu Asn Glu Phe Pro Gly Arg Gly Leu Asp Pro Leu Leu Lys Phe
245 250 255

Ser Glu Trp Trp His Glu Ala Gln Asn Asn Lys Lys Val Ala Glu Asn
260 265 270

Pro Tyr Asp Thr Lys Val Lys Lys Lys Leu Arg Lys Leu Gln Leu Thr
275 280 285

Pro Gly Phe Pro Asn Pro Ala Val Ala Asp Ala Tyr Leu Arg Pro Val
290 295 300

Val Asp Asp Ser Arg Gly Ser Phe Leu Trp Gly Lys Pro Asp Val Asp
305 310 315 320

Lys Ile Arg Glu Phe Cys Gln Arg Tyr Phe Gly Trp Asn Arg Met Lys
325 330 335

Thr Asp Glu Ser Leu Tyr Pro Val Leu Lys His Leu Asn Ala His Gln
340 345 350

Thr Gln Leu Arg Ile Asp Ser Phe Phe Arg Leu Ala Gln Gln Glu Lys
355 360 365

Gln Asp Ala Lys Leu Ile Lys Ser His Arg Leu Ser Arg Ala Val Thr
370 375 380

Cys Met Leu Arg Lys Glu Arg Glu Glu Lys Ala Pro Glu Leu Thr Lys
385 390 395 400

Val Thr Glu Ala Met Glu Lys Glu Phe Glu Leu Leu Asp Asp Ala Lys
405 410 415

Gly Lys Thr Gln Lys Arg Glu Leu Pro Tyr Lys Lys Glu Thr Ser Val
420 425 430

Pro Lys Arg Arg Arg Pro Ser Gly Asn Gly Gly Phe Leu Gly Asp Pro
435 440 445

Tyr Cys Ser Glu Ser Pro Gln Glu Ser Ser Cys Glu Asp Gly Glu Gly
450 455 460

Ser Ser Val Met Ser Ala Arg Gln Arg Ser Ala Ala Glu Ser Ser Lys
465 470 475 480

Ile Gly Cys Ser Asp Val Pro Asp Leu Val Arg Asp Ser Pro His Gly
485 490 495

Arg Gln Gly Cys Val Ser Thr Ser Ser Ser Asp Ser Glu Asp Gly Glu
500 505 510

Asp Lys Ala Lys Thr Val Leu Val Thr Ala Arg Pro Val Phe Gly Lys
515 520 525

Lys Arg Arg Lys Leu Lys Ser Met Lys Arg Arg Lys Lys Lys Thr
530 535 540

<210> 144

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 144

Met Gly Val Gln Gly Leu Trp Lys Leu Leu Glu Cys Ser Gly Arg Pro
1 5 10 15

Ile Asn Pro Gly Thr Leu Glu Gly Lys Ile Leu Ala Val Asp Ile Ser
20 25 30

Ile Trp Leu Asn Gln Ala Val Lys Gly Ala Arg Asp Arg Gln Gly Asn
35 40 45

Ala Ile Gln Asn Ala His Leu Leu Thr Leu Phe His Arg Leu Cys Lys
50 55 60

Leu Leu Phe Phe Arg Ile Arg Pro Ile Phe Val Phe Asp Gly Glu Ala
65 70 75 80

Pro Leu Leu Lys Arg Gln Thr Leu Ala Lys Arg Arg Gln Arg Thr Asp
85 90 95

Lys Ala Ser Asn Asp Ala Arg Lys Thr Asn Glu Lys Leu Leu Arg Thr
100 105 110

Phe Leu Lys Arg Gln Ala Ile Lys Ala Glu Arg Ile Ala Ala Thr Val
115 120 125

Thr Gly Gln Met Cys Leu Glu Ser Gln Glu Leu Leu Gln Leu Phe Gly
130 135 140

Ile Pro Tyr Ile Val Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Ile
145 150 155 160

Leu Asp Leu Thr Asp Gln Thr Ser Gly Thr Ile Thr Asp Asp Ser Asp
165 170 175

Ile Trp Leu Phe Gly Ala Arg His Val Tyr Lys Asn Phe Phe Ser Gln
180 185 190

Asn Lys His Val Glu Tyr Tyr Gln Tyr Ala Asp Ile His Asn Gln Leu
195 200 205

Gly Leu Asp Arg Ser Lys Leu Ile Asn Leu Ala Tyr Leu Leu Gly Ser
210 215 220

Asp Tyr Thr Glu Gly Ile Pro Thr Val Gly Tyr Val Ser Ala Met Glu
225 230 235 240

Ile Leu Asn Glu Phe Pro Gly Gln Gly Leu Glu Pro Leu Val Lys Phe
245 250 255

Lys Glu Trp Trp Ser Glu Ala Gln Lys Asp Lys Lys Met Arg Pro Asn
260 265 270

Pro Asn Asp Thr Lys Val Lys Lys Lys Leu Arg Leu Leu Asp Leu Gln
275 280 285

Gln Ser Phe Pro Asn Pro Ala Val Ala Ser Ala Tyr Leu Lys Pro Val
290 295 300

Val Asp Glu Ser Lys Ser Ala Phe Ser Trp Gly Arg Pro Asp Leu Glu
305 310 315 320

Gln Ile Arg Glu Phe Cys Glu Ser Arg Phe Gly Trp Tyr Arg Leu Lys
325 330 335

Thr Asp Glu Val Leu Leu Pro Val Leu Lys Gln Leu Asn Ala Gln Gln
340 345 350

Thr Gln Leu Arg Ile Asp Ser Phe Phe Arg Leu Glu Gln His Glu Ala
355 360 365

```
Ala Gly Leu Lys Ser Gln Arg Leu Arg Arg Ala Val Thr Cys Met Lys
    370                 375                 380

Arg Lys Glu Arg Asp Val Glu Ala Glu Glu Val Glu Ala Ala Val Ala
385                 390                 395                 400

Val Met Glu Arg Glu Cys Thr Asn Gln Arg Lys Gly Gln Lys Thr Asn
                405                 410                 415

Thr Lys Ser Gln Gly Thr Lys Arg Arg Lys Pro Thr Glu Cys Ser Gln
            420                 425                 430

Glu Asp Gln Asp Pro Gly Gly Gly Phe Ile Gly Ile Glu Leu Lys Thr
        435                 440                 445

Leu Ser Ser Lys Ala Tyr Ser Ser Asp Gly Ser Ser Ser Asp Ala Glu
    450                 455                 460

Asp Leu Pro Ser Gly Leu Ile Asp Lys Gln Ser Gln Ser Gly Ile Val
465                 470                 475                 480

Gly Arg Gln Lys Ala Ser Asn Lys Val Glu Ser Ser Ser Ser Ser Asp
                485                 490                 495

Asp Glu Asp Arg Thr Val Met Val Thr Ala Lys Pro Val Phe Gln Gly
            500                 505                 510

Lys Lys Thr Lys Ser Lys Thr Met Lys Glu Thr Val Lys Arg Lys
        515                 520                 525
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<210> 145

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 145

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Met Thr Ile Asn Gly Ile Trp Glu Trp Ala Asn His Val Val Arg Lys
1               5                   10                  15

Val Pro Asn Glu Thr Met Arg Asp Lys Thr Leu Ser Ile Asp Gly His
            20                  25                  30

Ile Trp Leu Tyr Glu Ser Leu Lys Gly Cys Glu Ala His His Gln Gln
        35                  40                  45

Thr Pro Asn Ser Tyr Leu Val Thr Phe Phe Thr Arg Ile Gln Arg Leu
    50                  55                  60

Leu Glu Leu Lys Ile Ile Pro Ile Val Val Phe Asp Asn Ile Asn Ala
65                  70                  75                  80

Ser Ser Ser Ala His Glu Ser Lys Asp Gln Asn Glu Phe Val Pro Arg
                85                  90                  95
```

```
Lys Arg Arg Ser Phe Gly Asp Ser Pro Phe Thr Asn Leu Val Asp His
            100                 105                 110

Val Tyr Lys Thr Asn Ala Leu Leu Thr Glu Leu Gly Ile Lys Val Ile
        115                 120                 125

Ile Ala Pro Gly Asp Gly Glu Ala Gln Cys Ala Arg Leu Glu Asp Leu
    130                 135                 140

Gly Val Thr Ser Gly Cys Ile Thr Thr Asp Phe Asp Tyr Phe Leu Phe
145                 150                 155                 160

Gly Gly Lys Asn Leu Tyr Arg Phe Asp Phe Thr Ala Gly Thr Ser Ser
                165                 170                 175

Thr Ala Cys Leu His Asp Ile Met His Leu Ser Leu Gly Arg Met Phe
            180                 185                 190

Met Glu Lys Lys Val Ser Arg Pro His Leu Ile Ser Thr Ala Ile Leu
        195                 200                 205

Leu Gly Cys Asp Tyr Phe Gln Arg Gly Val Gln Asn Ile Gly Ile Val
    210                 215                 220

Ser Val Phe Asp Ile Leu Gly Glu Phe Gly Asp Asp Gly Asn Glu Glu
225                 230                 235                 240

Ile Asp Pro His Val Ile Leu Asp Arg Phe Ala Ser Tyr Val Arg Glu
                245                 250                 255

Glu Ile Pro Ala Arg Ser Glu Asp Thr Gln Arg Lys Leu Arg Leu Arg
            260                 265                 270

Arg Lys Lys Tyr Asn Phe Pro Val Gly Phe Pro Asn Cys Asp Ala Val
        275                 280                 285

His Asn Ala Ile Thr Met Tyr Leu Arg Pro Pro Val Ser Ser Glu Ile
    290                 295                 300

Pro Lys Ile Ile Pro Arg Ala Ala Asn Phe Gln Gln Val Ala Glu Ile
305                 310                 315                 320

Met Met Lys Glu Cys Gly Trp Pro Ala Thr Arg Thr Gln Lys Glu Leu
                325                 330                 335

Ala Leu Ser Ile Arg Arg Lys Val His Leu Thr Thr Thr Val Ala Gln
            340                 345                 350

Thr Arg Ile Pro Asp Phe Phe Ala Ala Thr Lys Ser Lys Asn Phe Thr
        355                 360                 365

Pro Ile Val Glu Pro Cys Glu Ser Leu Glu Asp Tyr Ile Ser Ala Asn
    370                 375                 380

Asn Thr Trp Met Arg Lys Arg Lys Arg Ser Glu Ser Pro Gln Ile Leu
385                 390                 395                 400
```

Gln His His Ala Lys Arg Gln Val Pro Asp Arg Lys Arg Ser Val Lys
405 410 415

Ile Arg Ala Phe Lys Pro Tyr Pro Thr Asp Val Ile Glu Leu Gly Asp
420 425 430

Ser Asp

<210> 146

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 146
tactgactca ctatagggtc ttctatggag gtc 33

<210> 147

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 147
ttttttttta attaggctct ggaagacgct gaaagcgtct tg 42

<210> 148

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 148
ttttttttta attaggctct ggaagacgga acgtcttg 38

<210> 149

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 149
ttttttttta attaggctct ggaagagaat cttg 34

<210> 150

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 150
ttttttttta attaggctct ggaaggaact tg 32

<210> 151

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 151
ttttttttta attaggctct ggaag 25

<210> 152

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position has a TET label.

<400> 152
attagaaagg aagggaagaa agcgaa 26

<210> 153

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 153
acggggaaag ccggcgaacg tggcgagaaa 30

<210> 154

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 154
tgacggggaa agccggcgaa cgtggcgaga 30

<210> 155

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 155
cttgacgggg aaagccggcg aacgtggcga 30

<210> 156

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 156
gcttgacggg gaaagccggc gaacgtggcg 30

<210> 157

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> The residue at this position contains a fluorescein label.

<400> 157
agaaaggaag ggaagaaa 18

<210> 158

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position contains a fluorescein label.

<400> 158
tggaggtcaa aacatcgata agtcgaagaa aggaagggaa gaaat 45

<210> 159

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position contains a fluorescein label.

<400> 159
tgttttgacc tcca 14

<210> 160

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 160
acacagtgtc ctcccgctcc tcctgagcaa 30

<210> 161

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position contains a fluorescein label.

<400> 161
tttccctcct cctcttcc 18

<210> 162

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 162
atgaggaaga ggaggagggt gctcaggagg agcgggagga cactgtgtct gtca 54

<210> 163

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 163
ttcgctttct tcccttcctt tctcgccacg ttcgccggct ttccccgtca agc 53

<210> 164

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 164
atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtacttctca 60

ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120

cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180

atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtgtt tgtattcgac 240

ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggctgag 300

gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360

caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct tttaagttac 420

atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480

gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc 540

ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc 600

tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg 660

acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg 720

aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg 780

gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg 840

aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc 900

atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttggag 960

aagctcaaag ctctgaagtc aacccaggcc acgcttgaga ggtggttctg a 1011

<210> 165

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 165

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Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1               5                  10                  15

Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
            20                  25                  30

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
        35                  40                  45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
    50                  55                  60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65                  70                  75                  80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
                85                  90                  95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
            100                 105                 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
        115                 120                 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
    130                 135                 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145                 150                 155                 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
                165                 170                 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
            180                 185                 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
        195                 200                 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
    210                 215                 220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
225                 230                 235                 240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
                245                 250                 255
```

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
260 265 270

Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
275 280 285

Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
290 295 300

Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
305 310 315 320

Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
325 330 335

<210> 166

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 166
ccgtcaacat ttaccatggg tgcgga 26

<210> 167

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 167
ccgccacctc gtagtcgaca tccttttcgt g 31

<210> 168

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 168
ggcgaccaca cccgtcctgt 20

<210> 169

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 169
ccacgatgcg tccggcgtag 20

<210> 170

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (29)..(29)

<223> The residue at this position is a 3' amine.

<400> 170
aacgaggcgc acccacccaa ggcacagcn 29

<210> 171

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 171
acgggtcaat gtccatgccc caaaga 26

<210> 172

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (23)..(27)

<223> The residues at these positions are 2'-O-methyls.

<220>

<221> modified_base

<222> (28)..(28)

<223> The residue at this position is a 3' amine.

<400> 172
gtctgagatg aaagtgcgcc tcgttaan 28

<210> 173

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 173
tcttcgcaca tttcatctca gacgga 26

<210> 174

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(21)

<223> The residues at these positions are 2'-O-methyls.

<220>

<221> modified_base

<222> (22)..(22)

<223> The residue at this position is a 3' amine.

<400> 174
gctgtgcctt gggtgggtgc gn 22

<210> 175

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (29)..(29)

<223> The residue at this position is a 3' amine.

<400> 175
aacgaggcgc acccacccaa ggcacagcn 29

<210> 176

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 176
acgggtcaat gtccatgccc caaaga 26

<210> 177

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (23)..(27)

<223> The residues at these positions are 2'-O-methyls.

<220>

<221> modified_base

<222> (28)..(28)

<223> The residue at this position is a 3' amine.

<400> 177
gtctgagatg aaagtgcgcc tcgttaan 28

<210> 178

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> The residue at this position is linked to a spacer containing a f
luorescein label

<400> 178
tcttcgcaca tttcatctca gac 23

<210> 179

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(17)

<223> The residues at these positions are 2'-O-methyls.

<220>

<221> modified_base

<222> (18)..(18)

<223> The residue at this position is a 3' amine.

<400> 179
gctgtgcctt gggtgggn 18

<210> 180

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(19)

<223> The residues at these positions are 2'-O-methyls.

<220>

<221> modified_base

<222> (20)..(20)

<223> The residue at this position is a 3' amine.

<400> 180
gctgtgcctt gggtgggtgn 20

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(21)

<223> The residues at these positions are 2'-O-methyls.

<220>

<221> modified_base

<222> (22)..(22)

<223> The residue at this position is a 3' amine.

<400> 181
gctgtgcctt gggtgggtgc gn 22

<210> 182

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(22)

<223> The residues at these positions are 2'-O-methyls.

<220>

<221> modified_base

<222> (23)..(23)

<223> The residue at this position is a 3' amine.

<400> 182
gctgtgcctt gggtgggtgc gcn 23

<210> 183

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> The residue at this position is linked to a spacer containing a f
luorescein label

<220>

<221> modified_base

<222> (22)..(22)

<223> The residue at this position indicates 2'-O-methyl sugar.

<220>

<221> modified_base

<222> (42)..(42)

<223> The residue at this position is a 3' amine.

<400> 183
gtctgagatg aaagtgctcc cgcacccacc caaggcacag cn 42

<210> 184

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(17)

<223> The residues at these positions are 2'-O-methyl sugars.

<220>

<221> modified_base

<222> (18)..(18)

<223> The residue at this position is a 3' amine.

<400> 184
gctgtgcctt gggtgggn 18

<210> 185

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (29)..(29)

<223> The residue at this position is a 3' primer.

<400> 185
aacgaggcgc acccacccaa ggcacagcn 29

<210> 186

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 186
gctgtgcctt gggtgggtgc g 21

<210> 187

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (21)..(21)

<223> The residue at this position is a 3' amine.

<400> 187
gctgtgcctt gggtgggtgc n 21

<210> 188

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (15)..(20)

<223> The residues at these positions are 2'-O-methyl sugars.

<220>

<221> modified_base

<222> (21)..(21)

<223> The residue at this position is a 3' amine.

<400> 188
gctgtgcctt gggtgggtgc n 21

<210> 189

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(20)

<223> The residues at these positions are 2'-O-methyl sugars.

<220>

<221> modified_base

<222> (21)..(21)

<223> The residue at this position is a 3' amine.

<400> 189
gctgtgcctt gggtgggtgc n 21

<210> 190

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> The residue at this position is linked to a spacer containing a f
luorescein label

<400> 190
tcttcgcaca tttcatctca gacgga 26

<210> 191

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 191
ctgggcgcgg acatggagga cgtgcgcggc cgcctggtgc agtaccgcgg cgag 54

<210> 192

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 192
ctgggcgcgg acatggagga cgtgtgcggc cgcctggtgc agtaccgcgg cgag 54

<210> 193

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 193
cgcgatgccg atgacctgca gaagcgcctg gcagtgtacc aggccggggc ccgcga 56

<210> 194

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 194
cgcgatgccg atgacctgca gaagtgcctg gcagtgtacc aggccggggc ccgcga 56

<210> 195

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> cggtactgcaccaggcggccgct

<400> 195
cggtactgca ccaggcggcc gct 23

<210> 196

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 196
ccccggcctg gtacactgcc aggct 25

<210> 197

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 197
aacgaggcgc acgcacgtcc tccatgt 27

<210> 198

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (24)..(24)

<223> The residue at this position is linked to 2-amino deoxyadenosine.

<400> 198
gaacgaggcg cacacacgtc ctcctgt 27

<210> 199

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 199
aacgaggcgc acgcttctgc aggtcatc 28

<210> 200

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (20)..(20)

<223> The residue at this position is linked to 2-amino deoxyadenosine.

<400> 200
aacgaggcgc acacttctgc ggtcatc 27

<210> 201

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 201
cctcgtctcg gttttccgag acgagggtgc gcctcgttc 39

<210> 202

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 202
cccctgggga agagcagaga tatacgtc 28

<210> 203

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 203
gggctccaca cggcgactct catt 24

<210> 204

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 204
ggtgctccac ctggcacgta tatctctgct cttccccag 39

<210> 205

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 205
ggtgctccac ctggtacgta tatctctgct cttccccag 39

<210> 206

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 206
agctgttcgt gttctatgat catgagagtc gccgtgtgga gccccg 46

<210> 207

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 207
agctgttcgt gttctatgat gatgagagtc gccgtgtgga gccccg 46

<210> 208

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 208
aacgaacgcg caggccaggt ggagcattt 29

<210> 209

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 209
aacgaacgcg cagaccaggt ggagcac 27

<210> 210

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 210
ctccgtctcg gttttccgag acggagctgc gcgttcguuu 40

<210> 211

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 211
aagcacgcag cacgatcata gaacacgaac agttt 35

<210> 212

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 212
aagcacgcag caccatcata gaacacgaac agttt 35

<210> 213

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 213
acgcgtctcg gttttccgag acgcgtgtgc tgcgtgcuuu 40

<210> 214

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 214
gaaggtgtct gcgggagccg atttcatcat cacgcagctt ttctttgagg 50

<210> 215

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 215
gaaggtgtct gcgggagtcg atttcatcat cacgcagctt ttctttgagg 50

<210> 216

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 216
caaagaaaag ctgcgtgatg atgaaatcgc 30

<210> 217

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 217
aacgaggcgc acgctcccgc agacac 26

<210> 218

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 218
aacgaggcgc acactcccgc agacacc 27

<210> 219

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 219
cctcgtctcg gttttccgag acgagggtgc gcctcgttt 39

<210> 220

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 220
actgggagca ttgaggctcg ctgagagtca cttttattgg gaaccatagt t 51

<210> 221

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 221
actgggagca ttgaggcttg ctgagagtca cttttattgg gaaccatagt t 51

<210> 222

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 222
tatggttccc aataaaagtg actctcagct 30

<210> 223

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 223
aacgaggcgc acgagcctca atgctccc 28

<210> 224

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 224
aacgaggcgc acaagcctca atgctccc 28

<210> 225

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is a spacer bearing a Cy3 dye.

<400> 225
cctcgtctcg gttttccgag acgagggtgc gcctcgttt 39

<210> 226

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 226
tgaagtctag agaaagggtt gtacggctga ggtctggaga aatgggcatc tg 52

<210> 227

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 227
tttgaaatgt cacagggttc ctaacagcca ctcttccctg gatggg 46

<210> 228

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 228
agatgcccat ttctccagac ctcagccc 28

<210> 229

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 229
aagcacgcag cacgtacaac cctttctcta gacaaa 36

<210> 230

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 230
ctccgtctcg gttttccgag acggaggtgc tgcgtgcuuu 40

<210> 231

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 231
ccatccaggg aagagtggcc tgttt 25

<210> 232

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 232
aagcacgcag cacaggaacc ctgtgacat 29

<210> 233

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 233
taggttttga ggggcatggg gacggggttc agcctccagg gtccta 46

<210> 234

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 234
taggttttga ggggcatgag gacggggttc agcctccagg gtccta 46

<210> 235

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 235
gaccctggag gctgaacccc gtcca 25

<210> 236

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 236
aacgaggcgc acccatcggg gtcaaaac 28

<210> 237

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 237
aacgaggcgc actcatgccc ctcaaaac 28

<210> 238

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 238
aaggacaaaa tacctgtatt cctcgcctgt ccagggatct gctcttacag attaga 56

<210> 239

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 239
aaggacaaaa tacctgtatt ccttgcctgt ccagggatct gctcttacag attaga 56

<210> 240

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (28)..(28)

<223> The residue at this position is linked to a purine.

<400> 240
taatctgtaa gagcagatcc ctggacagcc 30

<210> 241

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 241
aacgaggcgc acgaggaata caggtatttt gtc 33

<210> 242

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 242
aacgaggcgc acaaggaata caggtatttt gtc 33

<210> 243

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 243
ggtaaaggtt ggcaaaaaga taac 24

<210> 244

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 244
gcgccgaggt cttggggtgg ttacaag 27

<210> 245

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 245
tctcgtctcg gttttccgag actgagacct cggcgcg 37

<210> 246

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 246
cacttgcttc aggaccatat ttctctctc 29

<210> 247

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 247
cgcgccgagg acacctttt tagggtgctt tgt 33

<210> 248

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 248
aaaatcgatg gtaaaggttg gc 22

<210> 249

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 249
agttctgcag taccggattt gc 22

<210> 250

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 250
tcgctactag ttgcttagtg 20

<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 251
gtaaacataa gcaactttag 20

<210> 252

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 252
cttgtaacca ccccaagatt atctttttgc caacctttac c 41

<210> 253

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 253
acaaagcacc ctaaaaaagg tgtagagaga aatatggtcc tgaagcaagt g 51